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(54) PROCEDE D'ANALYSE DE PROTEINES

(54) PROTEIN ANALYSIS METHOD

(57)

It is intended to provide a protein analysis method whereby proteins can be identified and the quantification data can be obtained by a convenient procedure. Namely, a protein analysis method characterized by comprising: the step of cleaving two protein-containing samples individually with restriction enzymes at specific amino acid sites to give peptide chain-containing samples; the step of modifying peptide chains contained in the peptide chain-containing samples with labeling compounds having different masses due to isotopes so as to impart different masses to the peptide chains; the step of mixing the isotope-labeled peptide chain-containing samples and fractionally quantifying the sample mixture for individual peptide chains so as to determine a content ratio; the step of selecting peptide chains to be subjected to amino acid sequence identification from the peptide chains and identifying the amino acid sequences of the peptide chains; the step of specifying proteins corresponding to the peptide chains; and the step of determining the content ratio of the thus specified proteins based on the fractional quantification data of the peptide chains.

